

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
White, David
MacBeth, Kyle J.

<120> 2786, A NOVEL HUMAN AMINOPEPTIDASE

<130> 5800-62

<140> US 09/443,795
<141> 1999-11-19

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 650
<212> PRT
<213> Homo sapiens

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Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
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Ala Phe Glu Leu Leu His Leu Asp Leu Arg Ala Glu Phe Gly
35 40 45
Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
50 55 60
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
65 70 75 80
Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu
85 90 95
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
100 105 110
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
115 120 125
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
130 135 140
Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
145 150 155 160
Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
165 170 175
Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
180 185 190
Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser
195 200 205
Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln
210 215 220
Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser
225 230 235 240
Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile
245 250 255

Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala
 260 265 270
 Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu
 275 280 285
 Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys
 290 295 300
 Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala
 305 310 315 320
 Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val
 325 330 335
 Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met
 340 345 350
 Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr
 355 360 365
 Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp
 370 375 380
 Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu
 385 390 395 400
 Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys
 405 410 415
 Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp
 420 425 430
 Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg
 435 440 445
 Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro
 450 455 460
 Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp
 465 470 475 480
 Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser
 485 490 495
 Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp
 500 505 510
 Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser
 515 520 525
 Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln
 530 535 540
 Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr
 545 550 555 560
 Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly
 565 570 575
 Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys
 580 585 590
 Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr
 595 600 605
 His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
 610 615 620
 Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
 625 630 635 640
 Val Gln Gln Ile Val Ala Pro Lys Gly Ser
 645 650

<210> 2
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 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (62)...(2011)

<221> misc_feature
<222> (1)...(3107)
<223> n = A,T,C or G

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Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro
1 5 10 15
ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg 157
Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg
20 25 30
gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg 205
Ala Phe Glu Leu Leu His Leu Asp Leu Arg Ala Glu Phe Gly
35 40 45
cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc 253
Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val
50 55 60
ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gag ctg cgg ctg 301
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu
65 70 75 80
gac tcg cac ccg tgc ctg gag gtg acg gcg gcg ctg cgg cgg gag 349
Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Leu Arg Arg Glu
85 90 95
cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg 397
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr
100 105 110
cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag 445
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln
115 120 125
ccc tgc cgc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc 493
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val
130 135 140
ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga 541
Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly
145 150 155 160
aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg 589
Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg
165 170 175
gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca 637
Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser
180 185 190

gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser 195 200 205	685
acc tgg gag aag aga ggt cca aat aag ttc ttc ttc cag atg tgt cag Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Gln Met Cys Gln 210 215 220	733
ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser 225 230 235 240	781
gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile 245 250 255	829
gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala 260 265 270	877
aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu 275 280 285	925
ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys 290 295 300	973
ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala 305 310 315 320	1021
gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val 325 330 335	1069
acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met 340 345 350	1117
tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr 355 360 365	1165
tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp 370 375 380	1213
atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu 385 390 395 400	1261
cca ggc gtt gac ccg gac acc tat aat gag acc ccc tac gag aaa Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys 405 410 415	1309

ggt ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp	420 425 430	1357
cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg	435 440 445	1405
agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro	450 455 460	1453
gag ctt aag aaa aag aga gtg gat atc att cca ggt ttt gag ttt gat Glu Leu Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp	465 470 475 480	1501
cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser	485 490 495	1549
cct ggg gac tca ctc atg aag cct gct gaa gag cta gcc caa ctg tgg Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp	500 505 510	1597
gca gcc gag gag ctg gac atg aag gcc att gaa gcc gtg gcc atc tct Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser	515 520 525	1645
ccc tgg aag acc tac cag ctg gtc tac ttc ctg gat aag atc ctc cag Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln	530 535 540	1693
aaa tcc cct ctc cct cct ggg aat gtg aaa aaa ctt gga gac aca tac Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr	545 550 555 560	1741
cca agt atc tca aat gcc cgg aat gca gag ctc cgg ctg cga tgg ggc Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly	565 570 575	1789
caa atc gtc ctt aag aac gac cac cag gaa gat ttc tgg aaa gtg aag Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys	580 585 590	1837
gag ttc ctg cat aac cag ggg aag cag aag tat aca ctt ccg ctg tac Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr	595 600 605	1885
cac gca atg atg ggt ggc agt gag gtg gcc cag acc ctc gcc aag gag His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu	610 615 620	1933
act ttt gca tcc acc gcc tcc cag ctc cac agc aat gtt gtc aac tat Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr	625 630 635 640	1981
gtc cag cag atc gtg gca ccc aag ggc agt tagaggctcg tgtgcattggc		2031

Val Gln Gln Ile Val Ala Pro Lys Gly Ser
645 650

ccctgcctct tcaggctctc caggcttca gaataattgt ttgttccaa attcctgttc 2091
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gagacagaga acctgcccac agctctcccc gctacaggct gcaggcactg cagggcagcg 2271
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aaaaaaaaa 2459

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<212> PRT
<213> Artificial Sequence

<220>
<223> Ribonucleoprotein Binding Site

<221> VARIANT
<222> 27
<223> Xaa = Any Amino Acid

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Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
20 25 30

<210> 4
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<212> PRT
<213> Artificial Sequence

<220>
<223> Nuclear Localization Motif

<400> 4
Lys Lys Lys
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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Ribnucleoprotein Binding Motif

<400> 5
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<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> potential catalytic site

<400> 6
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<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> potential catalytic site

<400> 7
Trp Leu Asn Glu
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